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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/804,060

DATE: 07/30/2001

TIME: 15:48:02

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Output Set: N:\CRF3\07302001\I804060.raw

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3 <110> APPLICANT: MOCKEL, BETTINA
4     FARWICK, MIKE
5     HERMANN, THOMAS
6     MARX, ACHIM
7     PFEFFERLE, WALTER
9 <120> TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE CITA GENE
11 <130> FILE REFERENCE: MAS/21123/279062
13 <140> CURRENT APPLICATION NUMBER: 09/804,060
14 <141> CURRENT FILING DATE: 2001-03-13
16 <150> PRIOR APPLICATION NUMBER: DE 100 42 740.5
17 <151> PRIOR FILING DATE: 2000-08-31
19 <150> PRIOR APPLICATION NUMBER: DE 101 08 463.3
20 <151> PRIOR FILING DATE: 2001-02-22
22 <160> NUMBER OF SEQ ID NOS: 5
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 2055
28 <212> TYPE: DNA
29 <213> ORGANISM: Corynebacterium glutamicum
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (201)..(1853)
34 <223> OTHER INFORMATION: cita-Gen
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37 tttctgtgtt tctcgaaact ttgagatccc gagtgttctg tgttgcttgt gggagtataa 60
39 ggtggcgcgt gtcacgcaca gaagtgtttg gtgcattgcc tgaggtagtg cgcaaaataa 120
41 gacttttgtg cattatgatc agaattgttg gcctgggact tcgcttcacg ctctgctgat 180
43 aatcgccccc gggggtagac atg tct gtt ggt gga tcc gac tgg aaa aac ttc 233
44                               Met Ser Val Gly Gly Ser Asp Trp Lys Asn Phe
45                               1           5           10
47 aag gag gtg gac atc att cgc ttt gct acc cga ata ctg gtg att caa 281
48 Lys Glu Val Asp Ile Ile Arg Phe Ala Thr Arg Ile Leu Val Ile Gln
49                               15           20           25
51 gtg gct acc gtc gcg ttg gtg gta gct att tgc acc gga att ttc gca 329
52 Val Ala Thr Val Ala Leu Val Val Ala Ile Cys Thr Gly Ile Phe Ala
53                               30           35           40
55 gtt ttg atg atg gat cag atg aaa act gag gcc gag cac aca gcg ctg 377
56 Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His Thr Ala Leu
57                               45           50           55
59 tcc atc gga cgt tcg gtg gca tcc aac ccg cag atc cgc gag gaa gta 425
60 Ser Ile Gly Arg Ser Val Ala Ser Asn Pro Gln Ile Arg Glu Glu Val
61 60                               65           70           75
63 gcg ctt gat act caa aca gga gca aac cca tcg gcc gaa gaa tta gcc 473
64 Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu Glu Leu Ala
65                               80           85           90
67 gat gga gat atc caa gcg gtt gca cag gcg gcc aat gaa cgc act gga 521
68 Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu Arg Thr Gly

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69          95          100          105
71 gct ttg ttt gtc gtt atc act gac ggt tta ggt atc cgc ctg tcc cac 569
72 Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg Leu Ser His
73          110          115          120
75 cca gat gag gaa cgt ctg ggg gag cag gtg agc act agc ttt gag gct 617
76 Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser Phe Glu Ala
77          125          130          135
79 gcc atg cgg ggt gaa gaa acc atg gcg tgg gag act ggg acc ctc ggt 665
80 Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly Thr Leu Gly
81 140          145          150          155
83 gcg tcc gcg cga gca aaa gtg cct atc ttt gcg ccg gat tct agt gtt 713
84 Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp Ser Ser Val
85          160          165          170
87 cca gtc ggt gag gtc agt gtt ggg ttt gag cga gac agt gtg tat tcc 761
88 Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser Val Tyr Ser
89          175          180          185
91 cgc ctg ccc atg ttc ctc gcc gcc ctt gct ctt att tct gtg ttg gga 809
92 Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser Val Leu Gly
93          190          195          200
95 atc ctt atc ggc gtg ggt gta gcc atg ggc atg cga cgc cgt tgg gaa 857
96 Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg Arg Trp Glu
97          205          210          215
99 cgc gtg acc ttg ggt ttg cag ccg gag gag cta gtg acc ctt gtg caa 905
100 Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr Leu Val Gln
101 220          225          230          235
103 aat cag act gca gtc atc gat ggc att gat gag ggc gtg ctg gcg ctg 953
104 Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val Leu Ala Leu
105          240          245          250
107 agc cca aac gga aca att ggg gtg cat aat gag cag gcg caa tcc atg 1001
108 Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala Gln Ser Met
109          255          260          265
111 att ggt gca ggt cct atg agt ggc agg acg ttg aaa gaa cta ggg ctt 1049
112 Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu
113          270          275          280
115 gac ctg ggt ctt gat ggc gtt gta ttg cat ggt cag cat ccg gaa acc 1097
116 Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His Pro Glu Thr
117          285          290          295
119 gtt gcc cat aac ggc agg atc ctc tat ctg gat ttc cac ccc gtg cgc 1145
120 Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His Pro Val Arg
121 300          305          310          315
123 cgt ggg gat caa gat tta ggc tac gtg gta acc atc cgc gat cgt acc 1193
124 Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg Asp Arg Thr
125          320          325          330
127 gac atc att gaa ctc agt gaa cgc ctc gac tct gtg cgc acc atg acc 1241
128 Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg Thr Met Thr
129          335          340          345
131 cac gca ctc cgc gcc cag cgc cac gag ttt gcc aac cgc atc cac acc 1289
132 His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg Ile His Thr
133          350          355          360

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135 gca aca ggg ctt atc gac gcc ggc cgc gtc cac gac gcg gca gag ttt 1337
136 Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala Ala Glu Phe
137      365      370      375
139 cta ggc gat ata tcc cgc aac ggg gga cag tca cat cca ttg atc gga 1385
140 Leu Gly Asp Ile Ser Arg Asn Gly Gly Gln Ser His Pro Leu Ile Gly
141 380      385      390      395
143 tca gcg cac ctg aat gaa gca ttt ttg agc tca ttt tta agt act gct 1433
144 Ser Ala His Leu Asn Glu Ala Phe Leu Ser Ser Phe Leu Ser Thr Ala
145      400      405      410
147 tct att tcg gca tct gaa aag ggc gtt agt ctg cgc atc aac tct gac 1481
148 Ser Ile Ser Ala Ser Glu Lys Gly Val Ser Leu Arg Ile Asn Ser Asp
149      415      420      425
151 acg ctg atc ctt ggc act gtt aaa gat cca gaa gat gta gca acc att 1529
152 Thr Leu Ile Leu Gly Thr Val Lys Asp Pro Glu Asp Val Ala Thr Ile
153      430      435      440
155 ttg ggt aat tta atc aac aat gcc atc gac gcc gcg gtg gca ggt gaa 1577
156 Leu Gly Asn Leu Ile Asn Asn Ala Ile Asp Ala Ala Val Ala Gly Glu
157      445      450      455
159 gcc cca cgg tgg att gag ctt acg ttg atg gat gat gcc gat acg ctg 1625
160 Ala Pro Arg Trp Ile Glu Leu Thr Leu Met Asp Asp Ala Asp Thr Leu
161 460      465      470      475
163 gtc att tct gtt gca gat tct ggt cct gga atc cca gag ggc gtg gat 1673
164 Val Ile Ser Val Ala Asp Ser Gly Pro Gly Ile Pro Glu Gly Val Asp
165      480      485      490
167 gta ttt gcc aca gcc acc cag ata gga gac tct gaa gat aat gaa cgc 1721
168 Val Phe Ala Thr Ala Thr Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg
169      495      500      505
171 acc cac ggg cat ggc att ggt cta aaa ctg tgc cgg gct ttg gct aga 1769
172 Thr His Gly His Gly Ile Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg
173      510      515      520
175 tca cat ggt ggc gat gtc tgg gtg att gat aga gga acc gaa gat ggc 1817
176 Ser His Gly Gly Asp Val Trp Val Ile Asp Arg Gly Thr Glu Asp Gly
177      525      530      535
179 gct gta ttt gga gtg aaa cta ccg gga gta atg gag taatggatca 1863
180 Ala Val Phe Gly Val Lys Leu Pro Gly Val Met Glu
181 540      545      550
183 aacacttaaa gttttagtaa ttgatgatga tttcgcgcgc gccggcattc acgcctccat 1923
185 cgttgatgcg tcccctggat tttcgggtgg cggtaccgcg cgtaccctcg cagaggcaaa 1983
187 aaccctgacg gccacatttt ccccggtatc cctacttggt gatgtctacc tccccgacgg 2043
189 cgatggcatt ga
192 <210> SEQ ID.NO: 2 2055
193 <211> LENGTH: 551
194 <212> TYPE: PRT
195 <213> ORGANISM: Corynebacterium glutamicum
197 <400> SEQUENCE: 2
198 Met Ser Val Gly Gly Ser Asp Trp Lys Asn Phe Lys Glu Val Asp Ile
199 1      5      10      15
201 Ile Arg Phe Ala Thr Arg Ile Leu Val Ile Gln Val Ala Thr Val Ala
202      20      25      30

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204 Leu Val Val Ala Ile Cys Thr Gly Ile Phe Ala Val Leu Met Met Asp
205          35          40          45
207 Gln Met Lys Thr Glu Ala Glu His Thr Ala Leu Ser Ile Gly Arg Ser
208          50          55          60
210 Val Ala Ser Asn Pro Gln Ile Arg Glu Glu Val Ala Leu Asp Thr Gln
211          65          70          75          80
213 Thr Gly Ala Asn Pro Ser Ala Glu Glu Leu Ala Asp Gly Asp Ile Gln
214          85          90          95
216 Ala Val Ala Gln Ala Ala Asn Glu Arg Thr Gly Ala Leu Phe Val Val
217          100          105          110
219 Ile Thr Asp Gly Leu Gly Ile Arg Leu Ser His Pro Asp Glu Glu Arg
220          115          120          125
222 Leu Gly Glu Gln Val Ser Thr Ser Phe Glu Ala Ala Met Arg Gly Glu
223          130          135          140
225 Glu Thr Met Ala Trp Glu Thr Gly Thr Leu Gly Ala Ser Ala Arg Ala
226          145          150          155          160
228 Lys Val Pro Ile Phe Ala Pro Asp Ser Ser Val Pro Val Gly Glu Val
229          165          170          175
231 Ser Val Gly Phe Glu Arg Asp Ser Val Tyr Ser Arg Leu Pro Met Phe
232          180          185          190
234 Leu Ala Ala Leu Ala Leu Ile Ser Val Leu Gly Ile Leu Ile Gly Val
235          195          200          205
237 Gly Val Ala Met Gly Met Arg Arg Arg Trp Glu Arg Val Thr Leu Gly
238          210          215          220
240 Leu Gln Pro Glu Glu Leu Val Thr Leu Val Gln Asn Gln Thr Ala Val
241          225          230          235          240
243 Ile Asp Gly Ile Asp Glu Gly Val Leu Ala Leu Ser Pro Asn Gly Thr
244          245          250          255
246 Ile Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro
247          260          265          270
249 Met Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp
250          275          280          285
252 Gly Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly
253          290          295          300
255 Arg Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp
256          305          310          315          320
258 Leu Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu
259          325          330          335
261 Ser Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala
262          340          345          350
264 Gln Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile
265          355          360          365
267 Asp Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser
268          370          375          380
270 Arg Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn
271          385          390          395          400
273 Glu Ala Phe Leu Ser Ser Phe Leu Ser Thr Ala Ser Ile Ser Ala Ser
274          405          410          415
276 Glu Lys Gly Val Ser Leu Arg Ile Asn Ser Asp Thr Leu Ile Leu Gly

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277          420          425          430
279 Thr Val Lys Asp Pro Glu Asp Val Ala Thr Ile Leu Gly Asn Leu Ile
280          435          440          445
282 Asn Asn Ala Ile Asp Ala Ala Val Ala Gly Glu Ala Pro Arg Trp Ile
283          450          455          460
285 Glu Leu Thr Leu Met Asp Asp Ala Asp Thr Leu Val Ile Ser Val Ala
286 465          470          475          480
288 Asp Ser Gly Pro Gly Ile Pro Glu Gly Val Asp Val Phe Ala Thr Ala
289          485          490          495
291 Thr Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg Thr His Gly His Gly
292          500          505          510
294 Ile Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg Ser His Gly Gly Asp
295          515          520          525
297 Val Trp Val Ile Asp Arg Gly Thr Glu Asp Gly Ala Val Phe Gly Val
298          530          535          540
300 Lys Leu Pro Gly Val Met Glu
301 545          550
305 <210> SEQ ID NO: 3
306 <211> LENGTH: 481
307 <212> TYPE: DNA
308 <213> ORGANISM: Corynebacterium glutamicum
310 <220> FEATURE:
311 <223> OTHER INFORMATION: citAint
313 <400> SEQUENCE: 3
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316 ccattggcat gcgacgccgt tgggaacgcg tgaccttggg tttgcagccg gaggagctag 180
317 tgaccttgt gcaaatcag actgcagtca tcgatggcat tgatgagggc gtgctggcgc 240
318 tgagcccaaa cggaacaatt ggggtgcata atgagcaggc gcaatccatg attggtgcag 300
319 gtcctatgag tggcaggacg ttgaaagaac tagggcttga cctgggtctt gatggcgttg 360
320 tattgcatgg tcagcatccg gaaaccgttg ccataacgg caggatcctc tatctggatt 420
321 tccaccccggt gcgccgtggg gatcaagatt taggctacgt ggtaaccatc cgcatcgta 480
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326 <211> LENGTH: 20
327 <212> TYPE: DNA
328 <213> ORGANISM: Corynebacterium glutamicum
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Primer citA-int1
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337 <210> SEQ ID NO: 5
338 <211> LENGTH: 20
339 <212> TYPE: DNA
340 <213> ORGANISM: Corynebacterium glutamicum
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Primer citA-int2
345 <400> SEQUENCE: 5
346 gtacgatcgc ggatggttac

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VERIFICATION SUMMARY

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